[said] the DNA nucleotide sequence[s] from which said each partial sequence is extracted;

[first selecting] means for selecting a plurality of mutually different partial sequences meeting said conditions from said plurality of partial sequences based on the results of said [detecting] determining means; and

[determining] means for [determining the] taking at least one pair [nucleotide sequences] of primers for each of said plurality of mutually different DNA nucleotide sequences, a plurality pairs of primers for said plurality of mutual different DNA nucleotide sequences from the results of said selecting capable of specifically [hybridizing] amplifying said pair of primers to [said] a plurality of hybridized DNA nucleotide sequences [based on the results of said first selecting means].

wherein said plurality of primers are automatically collated with genetic functions related to said DNA nucleotide sequences respectively from which they are extracted.

2.(Amended) A primer design system according to claim 1, said control unit further controls second [selecting] means for selecting a plurality of primers [DNA nucleotide sequences] meeting certain selection conditions from [the] said plurality of partial sequences extracted by said extracting means.

3.(Amended) A primer design system according to claim 2, said selection conditions [being related to] determine the range of GC content and/or Tm of DNA nucleotide sequences to be selected.

4.(Amended) A primer design system according to claim 1, said control unit further controls [limiting] means for limiting the plurality of mutually different DNA nucleotide sequences, the data for which were obtained by said [receiver] selecting means, to a base length longer than said [prescribed] certain base length, to be output to said extracting means.

5.(Amended) A primer design system according to claim 1, [said control unit] further [controls of] comprising [third selecting] means controlled by said control unit for selecting DNA nucleotide sequences meeting selection conditions [related to] of GC content and/or Tm [based on] from the plurality of DNA nucleotide sequences, based on the data [for which were] obtained by said [receiver] selecting means.

6.(Amended) A primer design system according to claim 1, further comprising a second database including data [for] on a plurality of different DNA nucleotide sequences, said second database comprising at least one of either data on cDNA nucleotide sequences included in said first database, or data on the exon nucleotide sequences predicted on the basis of genomic DNA nucleotide sequences included in said first database, wherein said extracting means targets nucleotide sequences included in said second database for extraction.

7.(Amended) A storage medium having recorded thereon a program executable at a control unit in a computer having said control unit and memory with data on a plurality of mutually different DNA nucleotide sequences, said program comprising instruction for reading data on a plurality of mutually different DNA nucleotide sequences in said memory, for extracting a plurality of partial sequences having a prescribed base length from said plurality of

DNA nucleotide sequences based on data on said plurality of DNA nucleotide sequences, for [detecting] determining [certain conditions related to] the positions of said plurality of partial sequences related to each one of said DNA nucleotide sequences and conditions of their absence in DNA nucleotide sequences other than said DNA nucleotide sequences, for selecting a plurality of mutually different partial sequences meeting said conditions, and for [determining the] taking at least one pair of nucleotide sequences of primers for each of said plurality of mutually different DNA nucleotide sequences, a plurality pairs of primers for said plurality of mutual different DNA nucleotide sequences from the results of said selecting means capable of [hybridizing] specifically amplifying said pair of primers to a [said] plurality of hybridized DNA nucleotide sequences [based on said selected partial sequences], wherein said plurality of primers are automatically collated with genetic functions related to said DNA nucleotide sequences respectively from which they are extracted.

8.(Amended) A method for designing primers, comprising the steps of taking data on a plurality of mutually different DNA nucleotide sequences from a database including a plurality of different DNA nucleotide sequences;

extracting a plurality of partial sequences having a certain base length from said plurality of DNA nucleotide sequences based on said nucleotide sequence data obtained above;

[detecting] determining [certain conditions related to] the positions of said plurality of partial sequences related to each one of said DNA nucleotide sequences, and conditions of their absence in DNA nucleotide sequences other than said DNA nucleotide sequences;

selecting a plurality of mutually different partial sequences meeting said conditions from said plurality of partial sequences based on said [detecting] determining results; [and]

[determining the] taking at least one pair of nucleotide sequences of primers for each of said plurality of mutually different DNA nucleotide sequences, a plurality pairs of primers for said plurality of mutual different DNA nucleotide sequences from the results of said selecting means capable of specifically [hybridizing] amplifying said pair of primers to [said] a plurality of hybridized DNA nucleotide sequences [based on said selected partial sequences], and

automatically collating said plurality of primers with genetic functions related to said DNA nucleotide sequences respectively from which they are extracted.

11. (Amended) A method for designing primers [analyzing DNA], comprising the [analysis] steps of taking data on a plurality of mutually different DNA nucleotide sequences from a database including a plurality of different DNA nucleotide sequences;

extracting a plurality of partial sequences having a certain base length from said plurality of DNA nucleotide sequences based on said nucleotide sequence data obtained above;

determining certain conditions related to the positions of said plurality of partial sequences related to each one of said DNA nucleotide sequences, and conditions of their absence in DNA nucleotide sequences other than said DNA nucleotide sequences;

selecting a plurality of mutually different partial sequences meeting said conditions from said plurality of partial sequences based on said determining results;

taking at least one pair of primers for each of said plurality of mutually different DNA nucleotide sequences, a plurality pairs of primers for said plurality of mutual different DNA nucleotide sequences from the results of said selecting means capable of specifically amplifying said pair of primers to a plurality of hybridized DNA nucleotide sequences; and

[analysis] analyzing a sample DNA using as an indicator the type of primer affording PCR amplified fragments among said plurality of primers, [using a DNA analysis kit] comprising a storage medium [according to claim 9] and plurality of primers, the data for which have been recorded on said storage medium,

wherein said storage medium comprising recorded data on said plurality of primers capable of specifically amplifying to mutually different DNAs, genetic data on DNA fragments amplified by PCR using said plurality of primers, and collating data between said plurality of primers and genetic functions related to said DNA nucleotide sequences from which they are extracted.

Please add new claim 13 as follows:

--~~13~~ 19. A primer design system, comprising:

means for selecting a mutually different plurality of mutually different DNA nucleotide sequences based on at least one predetermined genetic function of interest from a first database having data on a plurality of different DNA nucleotide sequences; and

a control unit for controlling the system, said control unit controlling:

means for extracting a plurality of partial sequences meeting certain base length extraction conditions from the plurality of DNA nucleotide sequences and the data of said genetic functions of interest;

means for determining the positions of said plurality of partial sequences related to each one of said DNA nucleotide sequences, and conditions of each partial sequence's absence in DNA nucleotide sequences other than the DNA nucleotide sequence from which said each partial sequence is extracted;

means for selecting a plurality of mutually different partial sequences meeting said conditions from said plurality of partial sequences based on the results of said determining means; and

means for taking at least one pair of primers for each of said plurality of mutually different DNA nucleotide sequences, a plurality pairs of primers for said plurality of mutual different DNA nucleotide sequences from the results of said selecting means capable of specifically amplifying said pair of primers to a plurality of hybridized DNA nucleotide sequences,

wherein said plurality of primers are automatically collated with said genetic functions of interest related to said DNA nucleotide sequences respectively from which they are extracted.--